

GUIDE TO AROMATIC AMINO-ACID BIOSYNTHESIS ACRONYMS

Functional Reaction ^a	Acronyms for Analog or Sub-homolog Types ^b	Query Tags (gi number)	Organisms
2-Keto-3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	AroA _{Iα} AroA _{Iβ} AroA _{II} *AroA _{II}	21646940 4980844 81555637 410486	<i>Chlorobium tepidum</i> (Ctep) <i>Thermotoga maritima</i> (Tmar) <i>Helicobacter pylori</i> (H pyl) <i>Lycopersicon esculentum</i> (Lesc)
2-Keto-3-deoxy-D-manno-octulosonate 8-phosphate (KDOP) synthase ^c	KdsA	67466688	<i>Escherichia coli</i> (Ecol)
2-Amino-3,7-dideoxy-D-threo-hept-6-ulosonate (ADTH) synthase	AroA'	1591105	<i>Methanococcus jannaschii</i> (Mjan)
Dehydroquinate synthase I	AroB *AroB	5822049 18425036	<i>Emericella nidulans</i> (Enid) <i>Arabidopsis thaliana</i> (Atha)
Dehydroquinate synthase II	AroB'	1591882	<i>Methanococcus jannaschii</i> (Mjan)

Dehydroquinase ^d	AroC _I *AroC _I •	17433709 15230703	<i>Salmonella typhimurium</i> (Styp) <i>Arabidopsis thaliana</i> (Ath)
	AroC _{II}	61219243	<i>Mycobacterium tuberculosis</i> (Mtub)
Shikimate dehydrogenase ^d	AroD •AroD	16131162 15230703	<i>Escherichia coli</i> (Ecol) <i>Arabidopsis thaliana</i> (Ath)
Shikimate kinase	AroE _I *AroE _I	114199 30692396	<i>Erwinia chrysanthemi</i> (Echr) <i>Arabidopsis thaliana</i> (Ath)
	AroE _{II}	14194467	<i>Methanococcus jannaschii</i> (Mjan)
Enolpyruvylshikimate-3-phosphate (EPSP) synthase	AroF *AroF	2506201 15225450	<i>Escherichia coli</i> (Ecol) <i>Arabidopsis thaliana</i> (Ath)
Chorismate synthase	AroG *AroG	114183 18402389	<i>Escherichia coli</i> (Ecol) <i>Arabidopsis thaliana</i> (Ath)
Anthranilate synthase (α subunit) [¥]	TrpAa *TrpAa	14973317 18410376	<i>Streptococcus pneumoniae</i> (Spne) <i>Arabidopsis thaliana</i> (Ath)
PABA synthase (α subunit) [¥]	PabAa *PabAa•	16129766 30684045	<i>Escherichia coli</i> (Ecol) <i>Arabidopsis thaliana</i> (Ath)

Anthranilate synthase (β subunit) ^Y	TrpAb *TrpAb	14973316 21594026	<i>Streptococcus pneumoniae</i> (Spne) <i>Arabidopsis thaliana</i> (Atha)
PABA ^e synthase (β subunit) ^Y	PabAb •PabAb	16131239 30684045	<i>Escherichia coli</i> (Ecol) <i>Arabidopsis thaliana</i> (Atha)
PABA synthase // Anthranilate synthase (β subunit)^Y	PabAb // TrpAb	129521	<i>Bacillus subtilis</i> (Bsub)
PABA synthase (γ subunit); 4-Amino-4-deoxy-chorismate lyase	PabAc *PabAc	1787338 22327924	<i>Escherichia coli</i> (Ecol) <i>Arabidopsis thaliana</i> (Atha)
Anthranilate Phosphoribosyl-transferase	TrpB *TrpB	14973315 15238711	<i>Streptococcus pneumoniae</i> (Spne) <i>Arabidopsis thaliana</i> (Atha)
Phosphoribosyl-anthranilate isomerase	TrpC _I *TrpC _I	14973313 30680348	<i>Streptococcus pneumoniae</i> (Spne) <i>Arabidopsis thaliana</i> (Atha)
PR-5-amino-1-PR-4-imidazole carboxamide // PR-anthranilate isomerase^e	HisD // TrpC_{II}	45593458	Mycobacterium tuberculosis (Mtub)
Indoleglycerol-phosphate synthase	TrpD *TrpD	14973314 15238914	<i>Streptococcus pneumoniae</i> (Spne) <i>Arabidopsis thaliana</i> (Atha)

Tryptophan synthase (α subunit)	TrpEa $_{\alpha}$ *TrpEa $_{\alpha}$	25291883 18410104	<i>Streptococcus pneumoniae</i> (Spne) <i>Arabidopsis thaliana</i> (Atha)
	TrpEa $_{\beta}$	004320	<i>Sulfolobus sulfataricus</i> (Ssul)
Tryptophan synthase (β subunit)	TrpEb $_{\alpha}$ *TrpEb $_{\alpha}$	25291905 15239755	<i>Streptococcus pneumoniae</i> (Spne) <i>Arabidopsis thaliana</i> (Atha)
	TrpEb $_{\beta}$	1004319	<i>Sulfolobus sulfataricus</i> (Ssul)
Chorismate mutase	AroH $_{\text{I}}$ *AroH $_{\text{I}}$	2495875 14794421	<i>Methanococcus jannaschii</i> (Mjan) <i>Pseudomonas aeruginosa</i> (Paer)
	AroH $_{\text{II}}$	24212657	<i>Bacillus subtilis</i> (Bsub)
	AroH $_{\text{III}}$ *AroH $_{\text{III}}$	6325317 18406100	<i>Saccharomyces cerevisiae</i> (Scer) <i>Arabidopsis thaliana</i> (Atha)
Arogenate dehydrogenase ‡	TyrA $_{\text{a}}$ *TyrA $_{\text{a}}$	62389124 15218283	<i>Corynebacterium glutamicus</i> (Cglu) <i>Arabidopsis thaliana</i> (Atha)
Prephenate dehydrogenase ‡	TyrA $_{\text{p}} \cdot \text{ACT}$	143815	<i>Bacillus subtilis</i> (Bsub)
Cyclohexadienyl dehydrogenase ‡	TyrA $_{\text{c}}$	56551316	<i>Zymomonas mobilis</i> (Zmob)

Prephenate dehydratase [¥]	PheA _{Iρ} •ACT	130048	<i>Bacillus subtilis</i> (Bsub)
Arogenate dehydratase [¥]	PheA _{Iα} •ACT *PheA _{Iα} •ACT	58000965 79317657	<i>Gluconobacter oxydans</i> (Goxy) <i>Arabidopsis thaliana</i> (Atha)
Cyclohexadienyl dehydratase	*PheA _{IIc}	2997758	<i>Pseudomonas aeruginosa</i> (Paer)
Aromatic aminotransferase	AroJ _{Iα}	85676806	<i>Escherichia coli</i> (Ecol)
	AroJ _{Iβ}	1574093	<i>Haemophilus influenzae</i> (Hinf)
	*AroJ _{Iβ}	14794424	<i>Pseudomonas aeruginosa</i> (Paer)
	AroJ _{Iγ}	6318592	<i>Lactococcus lactis</i> (Llac)

aEnzymes in a box that are marked with the symbol [¥] following the name currently cannot be distinguished from one another with great confidence using the query-tag sequences given.

bSpacing within a box indicates distinctly separated analog or sub-homolog groupings, with the exception of what is covered in footnote^a. Asterisk superscripts indicate signal peptides in prokaryotes, whereas green asterisk superscripts indicate transit peptides in higher plants.

cUse this query to assure that a putative AroA_{I β} sequence is not in fact a KdsA sequence.

dThe convention of a bullet indicates the fusion of the two indicated domains in *AroC_I•AroD proteins of higher plants.

eAbbreviations: PABA, 4-aminobenzoate; PR, phosphoribosyl.